Clonal clusters and virulence factors of methicillin-resistant Staphylococcus aureus

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Title: Clonal clusters and virulence factors of methicillin-resistant : Evidence for community-acquired methicillin-resistant infiltration into hospital settings in Chennai, South India.

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Abstract: <bold>Background and Objective: </bold>Staphylococcus aureus is one of the major pathogens of nosocomial infections as wells as community-acquired (CA) infections worldwide. So far, large-scale comprehensive molecular and epidemiological characterisation of S. aureus from very diverse settings has not been carried out in India. The objective of this study is to evaluate the molecular, epidemiological and virulence characteristics of S. aureus in both community and hospital settings in Chennai, southern India. <bold>Methods: </bold>S. aureus isolates were obtained from four different groups (a) healthy individuals from closed community settings, (b) inpatients from hospitals, (c) outpatients from hospitals, representing isolates of hospital-community interface and (d) HIV-infected patients to define isolates associated with the immunocompromised. Antibiotic susceptibility testing, multiplex polymerase chain reactions for detection of virulence and resistance determinants, molecular typing including Staphylococcal cassette chromosome mec (SCCmec) and agr typing, were carried out. Sequencing-based typing was done using spa and multilocus sequence typing (MLST) methods. Clonal complexes (CC) of hospital and CA methicillin-resistant S. aureus (MRSA) were identified and compared for virulence and resistance.<bold>Results

and Conclusion: </bold>A total of 769 isolates of S. aureus isolates were studied. The prevalence of MRSA was found to be 7.17%, 81.67%, 58.33% and 22.85% for groups a, b, c and d, respectively. Of the four SCCmec types (I, III, IV and V) detected, SCCmec V was found to be predominant. Panton-Valentine leucocidin toxin genes were detected among MRSA isolates harbouring SCCmec IV and V. A total of 78 spa types were detected, t657 being the most prevalent. 13 MLST types belonging to 9 CC were detected. CC1 (ST-772, ST-1) and CC8 (ST238, ST368 and ST1208) were found to be predominant among MRSA. CA-MRSA isolates with SCCmec IV and V were isolated from all study groups including hospitalised patients and were found to be similar by molecular tools. This shows that CA MRSA has probably infiltrated into the hospital settings. [ABSTRACT FROM AUTHOR]

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